Imperial College London

FullMvaToolkit (FMT) Running Instructions

Matthew Kenzie

May 27, 2012

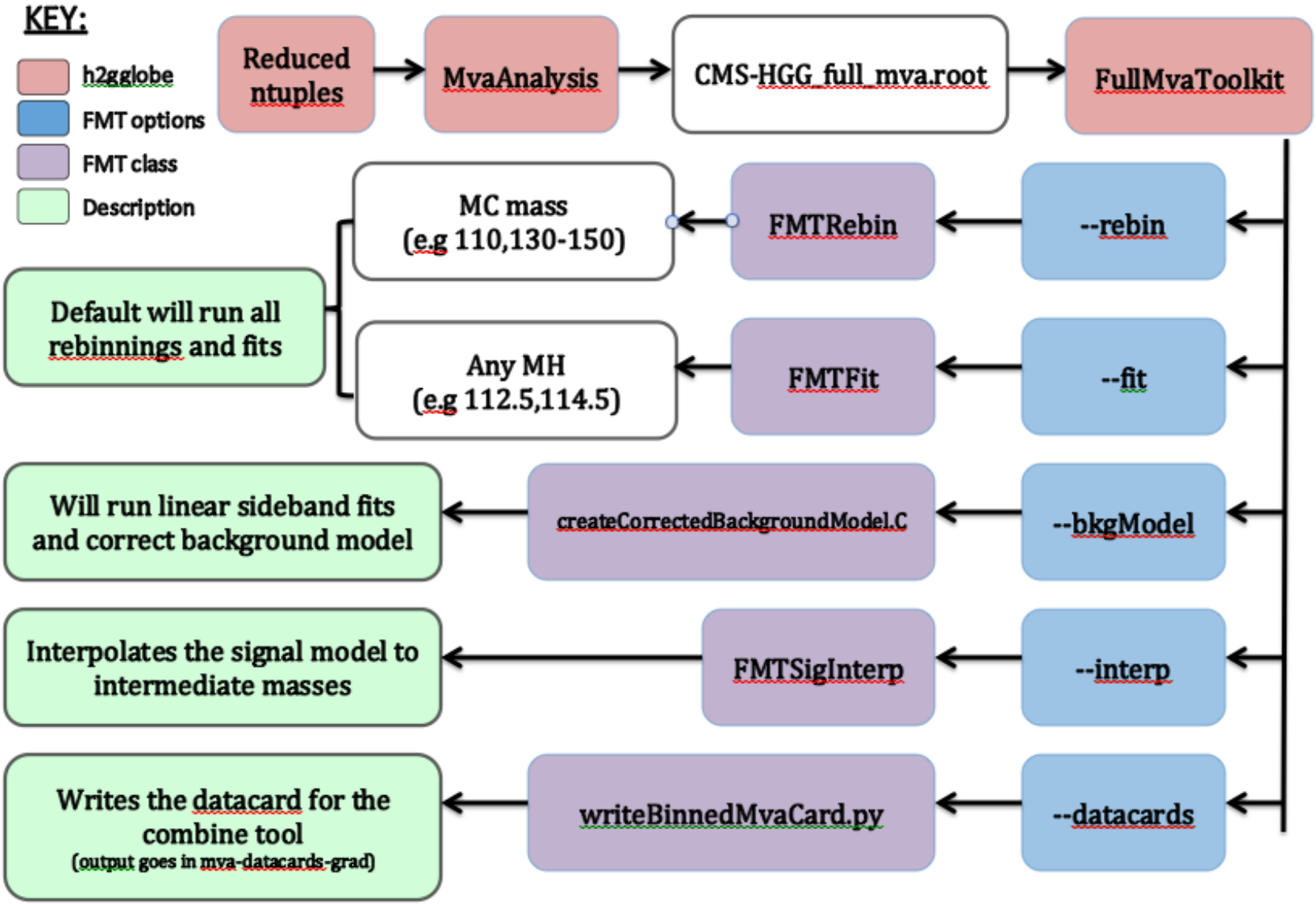
Introduction

- These slides can serve as a reference and instructions on how to run the `FullMvaToolkit`
- Check out the head of `h2gglobe` and find the package under:
  `h2gglobe/Macros/FullMvaToolkit`
- After running `MvaAnalysis`:
  - `cd FullMvaToolkit` and `make`
  - `./runIt.exe --help` to see list of options
  - Run `subFMTBatch.sh` to execute the full chain in the recommended way - takes $\approx \frac{1}{2}$ hour.
- Detailed workflow on next two slides.
- Would be great if someone could independently test the changes that have been made to both `MvaAnalysis`and `FullMvaToolkit`
  - i.e. run the full chain (`fitter.py` + `FullMvaToolkit`)

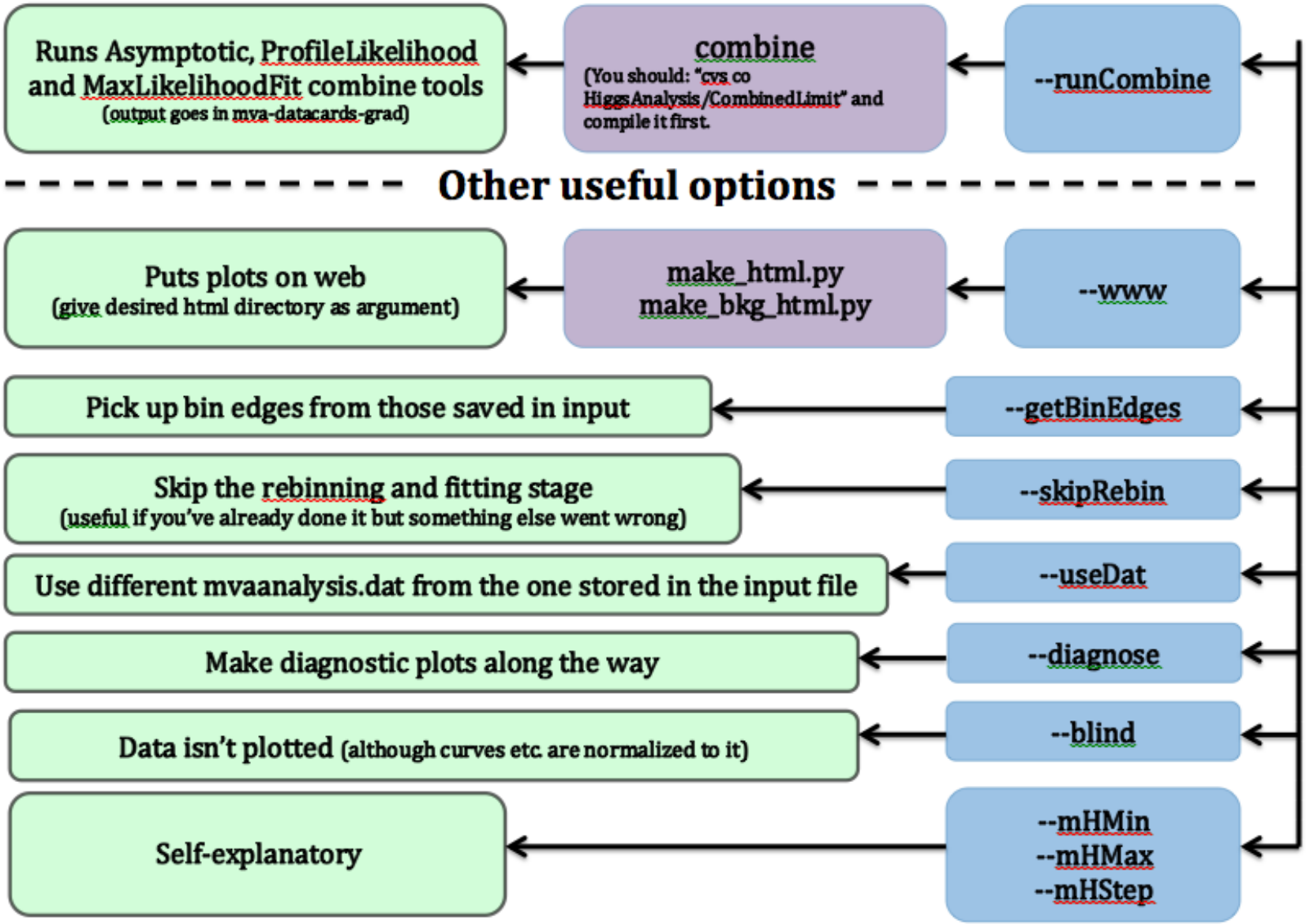
Updates w.r.t previous framework

- `MvaAnalysis`
  - Now inheritence structure from baseline (`StatAnalysis`) and mass factorized (`MassFactorizedMvaAnalysis`).
  - Analysis now essentially done by AnalyzeEvent() method
  - There is no seperaete VBF - each additional tag is added as a category.
  - Now allows specifying m_H in different steps and ranges.
  - Rebinning and fitting is not done here.
- `FullMvaToolkit`
  - Rebinning and fitting done here.
  - Allows merging of inclusive categories with exclusive categories:
    multiple VBF cats / VBF and LEP cats
  - Combines lots of old macros into one coherent piece.
  - Lots of versatility - can run anyone of several bits of the analysis just by passing different command line options.

Workflow (part 1)



Workflow (part 2)



Further work

- Integrate makefile with h2gglobe makefile - *high priority*
- Provide option and call to class which runs bias study - *medium priority*
- Tidy diagnostics plots and webpage - *low priority*